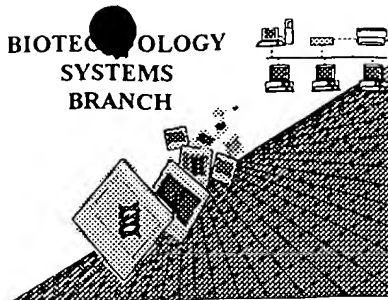


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



BC
#7

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/743,647

Source: O I P E

Date Processed by STIC: 07/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/743,647

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 / Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 07/26/2001

PATENT APPLICATION: US/09/743,647

TIME: 10:50:58

Input Set : A:\542683_1.txt

Output Set: N:\CRF3\07262001\I743647.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Pangalos, Menelas
 4 Neefs, Jean-Marc
 5 Peeters, Danielle
 7 <120> TITLE OF INVENTION: Cloning and Characterisation of Novel Mammalian Peptidases
 9 <130> FILE REFERENCE: J0205/7000 (JRV)
 11 <140> CURRENT APPLICATION NUMBER: 09/743,647
 ✓ C--> 12 <141> CURRENT FILING DATE: 2001-07-02
 14 <150> PRIOR APPLICATION NUMBER: GB 9815284.6
 15 <151> PRIOR FILING DATE: 1999-07-14
 17 <160> NUMBER OF SEQ ID NOS: 59
 19 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 35
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial Sequence ✓
 W--> 26 <220> FEATURE:
 W--> 26 <223> OTHER INFORMATION: ✓ Field 220 introduces the fields used to describe
 26 <400> SEQUENCE: 1 artificial sequences. When artificial sequences are
 27 cccggatccg agatgtggat tctccttcac gaaac present fields 220 and 223 are mandatory.
 30 <210> SEQ ID NO: 2 Field 223 requires requisite description
 31 <211> LENGTH: 36
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Artificial Sequence
 W--> 35 <220> FEATURE:
 W--> 35 <223> OTHER INFORMATION:
 35 <400> SEQUENCE: 2
 36 cccctcgagt taggctactt cactcaaagt ctctgc 36
 39 <210> SEQ ID NO: 3
 40 <211> LENGTH: 40
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Homo sapiens
 44 <400> SEQUENCE: 3
 45 ccctcagagt ggagcagctg ttgttcatga aattgtgagg 40
 48 <210> SEQ ID NO: 4
 49 <211> LENGTH: 40
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Homo sapiens
 53 <400> SEQUENCE: 4
 54 cctcacaatt tcatgaacaa cagctgctcc actctgaggg 40
 57 <210> SEQ ID NO: 5
 58 <211> LENGTH: 24
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Homo sapiens
 62 <400> SEQUENCE: 5
 63 gttcttcaac aagctgcagg agcg 24
 66 <210> SEQ ID NO: 6
 67 <211> LENGTH: 32

The types of errors shown exist throughout the Sequence Listing. Please check
 subsequent sequences for similar errors.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/743,647

DATE: 07/26/2001

TIME: 10:50:58

Input Set : A:\542683_1.txt

Output Set: N:\CRF3\07262001\I743647.raw

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68 <212> TYPE: DNA
69 <213> ORGANISM: Artificial Sequence
W--> 71 <220> FEATURE:
W--> 71 <223> OTHER INFORMATION:
71 <400> SEQUENCE: 6
72 cccctcgagc cggagtaaag ggagggctga ag 32
75 <210> SEQ ID NO: 7
76 <211> LENGTH: 24
77 <212> TYPE: DNA
78 <213> ORGANISM: Homo sapiens
80 <400> SEQUENCE: 7
81 ggcgacctga gcatctacga caac 24
84 <210> SEQ ID NO: 8
85 <211> LENGTH: 31
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
W--> 89 <220> FEATURE:
W--> 89 <223> OTHER INFORMATION:
89 <400> SEQUENCE: 8
90 cccctcgagt cccctcagag gtcagccaca g 31
93 <210> SEQ ID NO: 9
94 <211> LENGTH: 22
95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
98 <400> SEQUENCE: 9
99 gccagcaccc agagaaccca ag 22
102 <210> SEQ ID NO: 10
103 <211> LENGTH: 22
104 <212> TYPE: DNA
105 <213> ORGANISM: Homo sapiens
107 <400> SEQUENCE: 10
108 gctgcggttg aagtaccgga tc 22
111 <210> SEQ ID NO: 11
112 <211> LENGTH: 27
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
W--> 116 <220> FEATURE:
W--> 116 <223> OTHER INFORMATION:
116 <400> SEQUENCE: 11
117 ccataccta atacgactcact atagggc 27
120 <210> SEQ ID NO: 12
121 <211> LENGTH: 23
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
W--> 125 <220> FEATURE:
W--> 125 <223> OTHER INFORMATION:
125 <400> SEQUENCE: 12
126 actcactata gggctcgagc ggc 23
129 <210> SEQ ID NO: 13

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/743,647

DATE: 07/26/2001

TIME: 10:50:58

Input Set : A:\542683_1.txt

Output Set: N:\CRF3\07262001\I743647.raw

```

130 <211> LENGTH: 18
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
W--> 134 <220> FEATURE:
W--> 134 <223> OTHER INFORMATION:
134 <400> SEQUENCE: 13
135 tgtaaaacga cggccagt 18
138 <210> SEQ ID NO: 14
139 <211> LENGTH: 18
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
W--> 143 <220> FEATURE:
W--> 143 <223> OTHER INFORMATION:
143 <400> SEQUENCE: 14
144 caggaaacag ctatgacc 18
147 <210> SEQ ID NO: 15
148 <211> LENGTH: 25
149 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 15
153 ctgcagcttg ttgaactctt ctgtg 25
156 <210> SEQ ID NO: 16
157 <211> LENGTH: 24
158 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 16
162 caaacacgat tgatctgcga ggac 24
165 <210> SEQ ID NO: 17
166 <211> LENGTH: 29
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
W--> 170 <220> FEATURE:
W--> 170 <223> OTHER INFORMATION:
170 <400> SEQUENCE: 17
171 cggatatccg caggatgcag tggacgaag 29
174 <210> SEQ ID NO: 18
175 <211> LENGTH: 26
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
W--> 179 <220> FEATURE:
W--> 179 <223> OTHER INFORMATION:
179 <400> SEQUENCE: 18
180 caaacacaat tgatctgcga ggacgc 26
183 <210> SEQ ID NO: 19
184 <211> LENGTH: 26
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
W--> 188 <220> FEATURE:
W--> 188 <223> OTHER INFORMATION:

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/743,647

DATE: 07/26/2001

TIME: 10:50:58

Input Set : A:\542683_1.txt

Output Set: N:\CRF3\07262001\I743647.raw

```

188 <400> SEQUENCE: 19
189 gcgtcctcgc agatcaattg tgtttg                26
192 <210> SEQ ID NO: 20
193 <211> LENGTH: 25
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 20
198 ctttgatgat agcgcacaga agtgg                25
201 <210> SEQ ID NO: 21
202 <211> LENGTH: 21
203 <212> TYPE: DNA
204 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 21
207 ggaaagatgc cagcgagga c                    21
210 <210> SEQ ID NO: 22
211 <211> LENGTH: 26
212 <212> TYPE: DNA
213 <213> ORGANISM: Homo sapiens
215 <400> SEQUENCE: 22
216 cgtcagagcc gccctatcag attatc                26
219 <210> SEQ ID NO: 23
220 <211> LENGTH: 26
221 <212> TYPE: DNA
222 <213> ORGANISM: Homo sapiens
224 <400> SEQUENCE: 23
225 gaggagtttt ccaaagttgc agaccc                26
228 <210> SEQ ID NO: 24
229 <211> LENGTH: 23
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 24
234 gggaaacaaa caaatcagc ggc                    23
237 <210> SEQ ID NO: 25
238 <211> LENGTH: 28
239 <212> TYPE: DNA
240 <213> ORGANISM: Homo sapiens
242 <400> SEQUENCE: 25
243 gtcaaagtcc tggagtctct cactgaac                28
246 <210> SEQ ID NO: 26
247 <211> LENGTH: 23
248 <212> TYPE: DNA
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 26
252 gaccggagca agacttcagc cag                    23
255 <210> SEQ ID NO: 27
256 <211> LENGTH: 23
257 <212> TYPE: DNA
258 <213> ORGANISM: Homo sapiens
260 <400> SEQUENCE: 27

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/743,647

DATE: 07/26/2001

TIME: 10:50:58

Input Set : A:\542683_1.txt

Output Set: N:\CRF3\07262001\I743647.raw

```

261 gtgttgatat gcgttggccc aag 23
264 <210> SEQ ID NO: 28
265 <211> LENGTH: 31
266 <212> TYPE: DNA
267 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 28
270 cactaagaat aagaaaacag ataagtacag c 31
273 <210> SEQ ID NO: 29
274 <211> LENGTH: 33
275 <212> TYPE: DNA
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 29
279 gatcaacttg tataagtcgt ttatgaaaat ctg 33
282 <210> SEQ ID NO: 30
283 <211> LENGTH: 25
284 <212> TYPE: DNA
285 <213> ORGANISM: Homo sapiens
287 <400> SEQUENCE: 30
288 gcagaagaac aaggtggagt tgggtg 25
291 <210> SEQ ID NO: 31
292 <211> LENGTH: 24
293 <212> TYPE: DNA
294 <213> ORGANISM: Homo sapiens
296 <400> SEQUENCE: 31
297 gctttggatc catgacagtc atgg 24
300 <210> SEQ ID NO: 32
301 <211> LENGTH: 26
302 <212> TYPE: DNA
303 <213> ORGANISM: Homo sapiens
305 <400> SEQUENCE: 32
306 tgaaggtcgg agtcaacgga tttggt 26
309 <210> SEQ ID NO: 33
310 <211> LENGTH: 24
311 <212> TYPE: DNA
312 <213> ORGANISM: Homo sapiens
314 <400> SEQUENCE: 33
315 catgtgggcc atgaggtcca ccac 24
318 <210> SEQ ID NO: 34
319 <211> LENGTH: 2320
320 <212> TYPE: DNA
321 <213> ORGANISM: Homo sapiens
323 <220> FEATURE:
324 <221> NAME/KEY: Unsure
325 <222> LOCATION: (315)..(315)
326 <223> OTHER INFORMATION: n = a, c, g, or u/t
329 <400> SEQUENCE: 34
330 gccaagagtc cgcaggatgc agtggacgaa ggtgttgggg ctggggctgg gggctgctgc 60
332 cctcttgggg ctgggggatca tcctcgcca ctttgccatc cccaaaaaag ccaactcact 120
334 ggccccccag gacctggacc tggagatcct ggagaccgtc atggggcagc tggatgccca 180

```

Form
OK

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/743,647

DATE: 07/26/2001

TIME: 10:50:59

Input Set : A:\542683_1.txt

Output Set: N:\CRF3\07262001\I743647.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:26 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:35 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:35 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:71 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:71 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:89 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:179 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:188 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:188 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35